

# STN SEARCH HISTORY

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 10:40:59 ON 28 AUG 2006

L1 1357 SEA HAC1 OR HACA OR ERN4 OR IRE1 OR IREA OR ERN1  
L2 46 SEA (((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) HETEROLOGOUS)  
(P) SECRET?)  
L3 0 SEA L1 AND L2  
L4 0 SEA ((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) HETEROLOGOUS) AND  
L1  
L5 219 SEA ((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) HETEROLOGOUS)  
L6 22 SEA ((PROTEIN OR PEPTIDE OR POLYPEPTIDE) (W) SECRET?) AND L1  
L7 15 DUP REM L6 (7 DUPLICATES REMOVED)  
L8 2 SEA L7 AND PY<2001  
D L8,BIB,1-2  
D L8,ABS,1`  
D L8,ABS,2  
D L8,BIB,2  
L9 2634 SEA (UNFOLD? (A) PROTEIN (A) RESPONSE)  
L10 657 SEA L9 AND L1  
L11 123 SEA L10 AND (SECRET?)  
L12 56 DUP REM L11 (67 DUPLICATES REMOVED)  
L13 4 SEA L12 AND PY<2001  
D L13,BIB,1-4  
L14 4 SEA L13 AND (HAC1 OR HACA OR ERN4 OR IRE1 OR IREA OR ERN1)

## EAST Search History

| Ref # | Hits  | Search Query  | DBs   | Default Operator | Plurals | Time Stamp       |
|-------|-------|---|---|------------------|---------|------------------|
| L1    | 595   | Hac1 or HacA or Ern4 or IRe1 or IreA or Ern1                            | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:22 |
| L2    | 12779 | ((protein or peptide or polypeptide) with heterologous) same secret\$4) | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:36 |
| L3    | 85    | L1 and I2   | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:28 |
| L4    | 115   | unfold\$4 adj protein adj response                                      | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:28 |
| L5    | 21    | L4 and L2   | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:28 |
| L6    | 10    | L5 not I3   | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:31 |
| L7    | 47    | L4 and (heterologous with (protein or peptide or polypeptide))          | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:31 |
| L8    | 36    | L7 not L3   | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:31 |
| L9    | 26    | L8 not L6   | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:34 |
| L10   | 388   | L1 and (yeast or fungi or fungus)                                       | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:34 |
| L11   | 37    | L10 and (unfold\$4 adj protein adj response)                            | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND              | ON      | 2006/08/28 10:35 |

## EAST Search History

|     |    |  |   |     |    |                  |
|-----|----|--|---|-----|----|------------------|
| L12 | 21 | (unfold\$4 adj protein adj response)<br>and (((protein or peptide or<br>polypeptide) with heterologous)<br>same secret\$4) | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND | ON | 2006/08/28 10:36 |
| L13 | 10 | L12 not L1   | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND | ON | 2006/08/28 10:36 |
| L14 | 0  | L13 not L6   | US-PGPUB;<br>USPAT;<br>EPO; JPO;<br>DERWENT | AND | ON | 2006/08/28 10:36 |

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rup.

[Score Home](#)  
[Page](#)

[Retrieve Application](#)  
[List](#)

[SCORE System](#)  
[Overview](#)

[SCORE](#)  
[FAQ](#)

[Comments /](#)  
[Suggestions](#)

This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rup.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:19 ; Search time 150.72 Seconds  
(without alignments)  
392.788 Million cell updates/sec

Title: US-10-663-450-6\_COPY\_53\_116  
Perfect score: 324  
Sequence: 1 KKPAKKRKSWGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID           | Description        |
|------------|-------|---------------|--------|----|--------------|--------------------|
| 1          | 324   | 100.0         | 347    | 2  | Q5AQN3_EMENI | Q5aqn3 aspergillus |
| 2          | 324   | 100.0         | 350    | 2  | Q8TFU8_EMENI | Q8tfu8 emericella  |
| 3          | 321   | 99.1          | 348    | 2  | Q2U743_ASPOR | Q2u743 aspergillus |
| 4          | 317   | 97.8          | 342    | 2  | Q6W8X2_ASPNG | Q6w8x2 aspergillus |

|    |       |      |     |   |              |                    |
|----|-------|------|-----|---|--------------|--------------------|
| 5  | 315   | 97.2 | 433 | 2 | Q4WEY8_ASPFU | Q4wey8 aspergillus |
| 6  | 283   | 87.3 | 451 | 2 | Q8TFF3_TRIRE | Q8tff3 trichoderma |
| 7  | 282   | 87.0 | 430 | 2 | Q7SHF0_NEUCR | Q7shf0 neurospora  |
| 8  | 265   | 81.8 | 556 | 2 | Q2KH12_MAGGR | Q2kh12 magnaporthe |
| 9  | 250   | 77.2 | 429 | 2 | Q4HTT5_GIBZE | Q4htt5 gibberella  |
| 10 | 178.5 | 55.1 | 299 | 2 | Q6CEV1_YARLI | Q6cev1 yarrowia li |
| 11 | 174.5 | 53.9 | 273 | 2 | Q6CKQ1_KLULA | Q6ckq1 kluyveromyc |
| 12 | 171.5 | 52.9 | 230 | 1 | HAC1_YEAST   | P41546 saccharomyc |
| 13 | 171   | 52.8 | 260 | 2 | Q6BQC2_DEBHA | Q6bqc2 debaryomyce |
| 14 | 166   | 51.2 | 228 | 2 | Q75BQ5_ASHGO | Q75bq5 ashbya goss |
| 15 | 166   | 51.2 | 357 | 2 | Q5AA52_CANAL | Q5aa52 candida alb |
| 16 | 144   | 44.4 | 329 | 2 | Q6FLY3_CANGA | Q6fly3 candida gla |
| 17 | 117   | 36.1 | 336 | 2 | Q5VR11_ORYSA | Q5vrl1 oryza sativ |
| 18 | 116   | 35.8 | 168 | 1 | HY5_ARATH    | O24646 arabidopsis |
| 19 | 109   | 33.6 | 69  | 2 | Q58L60_BRACM | Q58l60 brassica ca |
| 20 | 109   | 33.6 | 109 | 2 | Q84XX8_BRARP | Q84xx8 brassica ra |
| 21 | 108   | 33.3 | 176 | 2 | Q69XK6_ORYSA | Q69xk6 oryza sativ |
| 22 | 105.5 | 32.6 | 141 | 2 | Q677A7_HYAOR | Q677a7 hyacinthus  |
| 23 | 104.5 | 32.3 | 252 | 2 | Q6NX18_XENTR | Q6nx18 xenopus tro |
| 24 | 103.5 | 31.9 | 158 | 1 | HY5_LYCES    | Q9sm50 lycopersico |
| 25 | 102.5 | 31.6 | 254 | 2 | Q2TAU5_XENLA | Q2tau5 xenopus lae |
| 26 | 102.5 | 31.6 | 350 | 2 | Q90ZR7_XENLA | Q90zr7 xenopus lae |
| 27 | 102.5 | 31.6 | 396 | 2 | Q7ZYC2_XENLA | Q7zyc2 xenopus lae |
| 28 | 100   | 30.9 | 208 | 2 | Q5DFK2_SCHJA | Q5dfk2 schistosoma |
| 29 | 100   | 30.9 | 321 | 2 | Q8GRY7_LOTJA | Q8gry7 lotus japon |
| 30 | 99    | 30.6 | 188 | 2 | Q6ZHT8_ORYSA | Q6zht8 oryza sativ |
| 31 | 98    | 30.2 | 120 | 2 | Q682B6_ARATH | Q682b6 arabidopsis |
| 32 | 98    | 30.2 | 149 | 1 | HYH_ARATH    | Q8w191 arabidopsis |
| 33 | 97    | 29.9 | 322 | 2 | Q39896_SOYBN | Q39896 glycine max |
| 34 | 97    | 29.9 | 326 | 2 | Q39895_SOYBN | Q39895 glycine max |
| 35 | 96    | 29.6 | 261 | 2 | Q3SZZ2_BOVIN | Q3szz2 bos taurus  |
| 36 | 95    | 29.3 | 703 | 2 | Q4WC74_ASPFU | Q4wc74 aspergillus |
| 37 | 94.5  | 29.2 | 309 | 2 | Q4H2M2_CIOIN | Q4h2m2 ciona intes |
| 38 | 94    | 29.0 | 322 | 2 | O04234_VICFA | O04234 vicia faba  |
| 39 | 94    | 29.0 | 627 | 2 | Q5BD44_EMENI | Q5bd44 aspergillus |
| 40 | 92    | 28.4 | 263 | 2 | Q8UVQ5_BRARE | Q8uvq5 brachydanio |
| 41 | 92    | 28.4 | 263 | 2 | Q90X27_BRARE | Q90x27 brachydanio |
| 42 | 92    | 28.4 | 383 | 2 | Q8QHJ5_BRARE | Q8qhj5 brachydanio |
| 43 | 92    | 28.4 | 383 | 2 | Q90XD3_BRARE | Q90xd3 brachydanio |
| 44 | 92    | 28.4 | 646 | 2 | Q6AU90_ORYSA | Q6au90 oryza sativ |
| 45 | 91.5  | 28.2 | 260 | 2 | Q6EZA7_OREMO | Q6eza7 oreochromis |

# ALIGNMENTS

## RESULT 1

Q5AQN3\_EMENI

ID Q5AQN3\_EMENI PRELIMINARY; PRT; 347 AA.

AC Q5AQN3;

DT 26-APR-2005, integrated into UniProtKB/TrEMBL.

DT 26-APR-2005, sequence version 1.

DT 07-MAR-2006, entry version 8.

DE Hypothetical protein.

GN ORFNames=AN9397.2;

OS Aspergillus nidulans FGSC A4.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; Emericella.

OX NCBI\_TaxID=227321;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

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This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450-6  
[start](#)

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:33:51 ; Search time 18.56 Seconds  
(without alignments)  
331.782 Million cell updates/sec

Title: US-10-663-450-6\_COPY\_53\_116  
Perfect score: 324  
Sequence: 1 KKPAAKKRKSQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | % Query |        | DB | ID     | Description        |
|------------|-------|---------|--------|----|--------|--------------------|
|            |       | Match   | Length |    |        |                    |
| 1          | 171.5 | 52.9    | 238    | 2  | S78571 | transcription fact |
| 2          | 116   | 35.8    | 168    | 2  | T50922 | bZIP protein HY5 [ |
| 3          | 97    | 29.9    | 322    | 2  | T08592 | TGACG-motif-bindin |
| 4          | 97    | 29.9    | 326    | 2  | T08591 | TGACG-motif bindin |
| 5          | 94    | 29.0    | 322    | 2  | T12093 | TGACG-motif bindin |
| 6          | 90.5  | 27.9    | 176    | 2  | B90087 | hypothetical prote |
| 7          | 90.5  | 27.9    | 506    | 2  | D84609 | hypothetical prote |
| 8          | 87.5  | 27.0    | 260    | 1  | A36299 | transcription fact |

|    |      |      |      |   |        |                    |
|----|------|------|------|---|--------|--------------------|
| 9  | 87.5 | 27.0 | 266  | 2 | JC7300 | tax-responsive ele |
| 10 | 87.5 | 27.0 | 267  | 2 | JC4857 | hepatocarcinogenes |
| 11 | 86   | 26.5 | 600  | 2 | T00759 | hypothetical prote |
| 12 | 83   | 25.6 | 688  | 2 | T32750 | hypothetical prote |
| 13 | 82.5 | 25.5 | 515  | 2 | A42140 | box B-binding fact |
| 14 | 82.5 | 25.5 | 516  | 2 | A44494 | cAMP-responsive el |
| 15 | 81   | 25.0 | 360  | 2 | T03373 | probable G-box bin |
| 16 | 81   | 25.0 | 468  | 2 | S33222 | transcription fact |
| 17 | 81   | 25.0 | 483  | 2 | S12741 | transcription fact |
| 18 | 79.5 | 24.5 | 486  | 2 | JC4028 | activating transcr |
| 19 | 77.5 | 23.9 | 1851 | 2 | T19964 | hypothetical prote |
| 20 | 77   | 23.8 | 433  | 2 | JC1230 | DNA-binding protei |
| 21 | 76.5 | 23.6 | 242  | 2 | S05453 | transcription fact |
| 22 | 76   | 23.5 | 207  | 2 | T40067 | hypothetical prote |
| 23 | 76   | 23.5 | 264  | 2 | T24253 | hypothetical prote |
| 24 | 76   | 23.5 | 331  | 2 | S33223 | transcription fact |
| 25 | 76   | 23.5 | 445  | 2 | T50972 | probable zuotin [i |
| 26 | 75.5 | 23.3 | 246  | 2 | T12585 | Dc3 promoter-bindi |
| 27 | 75.5 | 23.3 | 313  | 2 | A34785 | DNA-binding protei |
| 28 | 75.5 | 23.3 | 349  | 2 | A41349 | histone-specific t |
| 29 | 75.5 | 23.3 | 349  | 2 | S77570 | transcription fact |
| 30 | 75.5 | 23.3 | 351  | 2 | A45377 | transcription fact |
| 31 | 75.5 | 23.3 | 358  | 2 | C42026 | cyclic AMP respons |
| 32 | 75.5 | 23.3 | 389  | 1 | A39429 | cAMP response elem |
| 33 | 75.5 | 23.3 | 448  | 2 | A42026 | cAMP response elem |
| 34 | 75.5 | 23.3 | 456  | 2 | B42026 | cyclic AMP respons |
| 35 | 75.5 | 23.3 | 505  | 1 | S05380 | transcription fact |
| 36 | 75.5 | 23.3 | 849  | 1 | S64732 | scaffold attachmen |
| 37 | 75.5 | 23.3 | 1359 | 2 | T34036 | hypothetical prote |
| 38 | 75   | 23.1 | 381  | 2 | S26812 | transcription fact |
| 39 | 75   | 23.1 | 1549 | 1 | A40691 | trichohyalin - she |
| 40 | 74.5 | 23.0 | 313  | 2 | S66312 | G-box binding fact |
| 41 | 74.5 | 23.0 | 315  | 2 | S20883 | G-box-binding fact |
| 42 | 74.5 | 23.0 | 315  | 2 | G85433 | G-box-binding fact |
| 43 | 74.5 | 23.0 | 338  | 1 | TVMSFB | transforming prote |
| 44 | 74.5 | 23.0 | 338  | 2 | I53043 | transforming prote |
| 45 | 74.5 | 23.0 | 452  | 2 | H96710 | hypothetical prote |

# ALIGNMENTS

## RESULT 1

S78571

transcription factor HAC1 - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein YFL031w

C;Species: *Saccharomyces cerevisiae*

C;Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004

C;Accession: S78571; S56223; S53578

R;Murakami, Y.

submitted to the Protein Sequence Database, January 1998

A;Reference number: S78570

A;Accession: S78571

A;Molecule type: DNA

A;Residues: 1-238

A;Cross-references: UNIPROT:P41546; UNIPARC:UPI0000157F61; EMBL:D50617; MIPS:YFL031w

A;Note: this is a revision to the sequence from reference S56186

R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasa submitted to the EMBL Data Library, May 1995

A;Description: Analysis of the nucleotide sequence of chromosome VI from *Saccaromyces*

A;Reference number: S56186

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450- 6\_copy\_53\_116.rag.

|                            |                                      |                              |                       |                             |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| <a href="#">Score Home</a> | <a href="#">Retrieve Application</a> | <a href="#">SCORE System</a> | <a href="#">SCORE</a> | <a href="#">Comments /</a>  |
| <a href="#">Page</a>       | <a href="#">List</a>                 | <a href="#">Overview</a>     | <a href="#">FAQ</a>   | <a href="#">Suggestions</a> |

This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rag.

[start](#)

[Go Back to previous page](#)

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:15 ; Search time 133.12 Seconds  
(without alignments)  
219.816 Million cell updates/sec

Title: US-10-663-450-6\_COPY\_53\_116  
Perfect score: 324  
Sequence: 1 KKPAKKRKSWGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES



| Result No. | Score | % Match | Query Length | DB | ID       | Description        |
|------------|-------|---------|--------------|----|----------|--------------------|
| 1          | 324   | 100.0   | 349          | 8  | ADS12805 | Ads12805 Aspergill |
| 2          | 324   | 100.0   | 349          | 8  | ADS12803 | Ads12803 Aspergill |
| 3          | 324   | 100.0   | 349          | 8  | ADS12863 | Ads12863 Aspergill |
| 4          | 324   | 100.0   | 350          | 4  | AAB82976 | Aab82976 Aspergill |
| 5          | 324   | 100.0   | 350          | 5  | AAE15372 | Aae15372 Aspergill |
| 6          | 320   | 98.8    | 64           | 5  | AAE15374 | Aae15374 Aspergill |
| 7          | 317   | 97.8    | 342          | 4  | AAB82977 | Aab82977 Aspergill |
| 8          | 317   | 97.8    | 342          | 5  | AAE15381 | Aae15381 Aspergill |
| 9          | 317   | 97.8    | 342          | 8  | ADS12818 | Ads12818 Aspergill |
| 10         | 317   | 97.8    | 386          | 5  | AAE15379 | Aae15379 Aspergill |
| 11         | 317   | 97.8    | 386          | 8  | ADS12815 | Ads12815 Aspergill |
| 12         | 283   | 87.3    | 64           | 5  | AAE15373 | Aae15373 Trichoder |
| 13         | 283   | 87.3    | 450          | 4  | AAB82975 | Aab82975 Trichoder |
| 14         | 283   | 87.3    | 451          | 5  | AAE15371 | Aae15371 Trichoder |
| 15         | 283   | 87.3    | 451          | 8  | ADS12801 | Ads12801 Trichoder |
| 16         | 283   | 87.3    | 451          | 8  | ADS12804 | Ads12804 Trichoder |
| 17         | 277   | 85.5    | 409          | 7  | ABO43144 | Abo43144 A. thalia |
| 18         | 277   | 85.5    | 409          | 7  | ADB31925 | Adb31925 Plant (A. |
| 19         | 277   | 85.5    | 409          | 8  | ADO02271 | Ado02271 Thalecres |
| 20         | 171.5 | 52.9    | 84           | 5  | ABP02534 | Abp02534 Human ORF |
| 21         | 171.5 | 52.9    | 200          | 8  | ADS43437 | Ads43437 Bacterial |
| 22         | 171.5 | 52.9    | 230          | 2  | AAW53806 | Aaw53806 Transcrip |
| 23         | 171.5 | 52.9    | 230          | 8  | ADT87049 | Adt87049 Yeast Str |
| 24         | 171.5 | 52.9    | 238          | 2  | AAW53807 | Aaw53807 Transcrip |
| 25         | 170   | 52.5    | 68           | 5  | AAE15382 | Aae15382 Yeast HAC |
| 26         | 170   | 52.5    | 68           | 8  | ADS12859 | Ads12859 Saccharom |
| 27         | 116   | 35.8    | 168          | 5  | AAU93013 | Aau93013 Arabidops |
| 28         | 116   | 35.8    | 168          | 7  | ADD30174 | Add30174 Plant yie |
| 29         | 116   | 35.8    | 168          | 8  | ADI43893 | Adi43893 Plant tra |
| 30         | 116   | 35.8    | 211          | 3  | AAG08861 | Aag08861 Arabidops |
| 31         | 111.5 | 34.4    | 192          | 4  | AAB82614 | Aab82614 Maize roo |
| 32         | 111.5 | 34.4    | 192          | 4  | AAB82615 | Aab82615 Maize roo |
| 33         | 111.5 | 34.4    | 192          | 4  | AAB82616 | Aab82616 Maize roo |
| 34         | 111.5 | 34.4    | 192          | 4  | AAG66525 | Aag66525 Maize roo |
| 35         | 111.5 | 34.4    | 192          | 4  | AAG66526 | Aag66526 Maize roo |
| 36         | 109.5 | 33.8    | 185          | 9  | ADW17162 | Adw17162 Eucalyptu |
| 37         | 106.5 | 32.9    | 170          | 8  | ADM48147 | Adm48147 Polypepti |
| 38         | 106   | 32.7    | 163          | 9  | ADW17580 | Adw17580 Pinus rad |
| 39         | 100   | 30.9    | 143          | 3  | AAB33151 | Aab33151 Pinus rad |
| 40         | 98    | 30.2    | 120          | 3  | AAG27808 | Aag27808 Arabidops |
| 41         | 98    | 30.2    | 135          | 3  | AAG07181 | Aag07181 Arabidops |
| 42         | 98    | 30.2    | 149          | 3  | AAG07180 | Aag07180 Arabidops |
| 43         | 98    | 30.2    | 149          | 3  | AAG27807 | Aag27807 Arabidops |
| 44         | 98    | 30.2    | 188          | 3  | AAG27806 | Aag27806 Arabidops |
| 45         | 93.5  | 28.9    | 672          | 8  | ADX95805 | Adx95805 Plant ful |

#### ALIGNMENTS

##### RESULT 1

ADS12805

ID ADS12805 standard; protein; 349 AA.

XX

AC ADS12805;

XX

DT 16-DEC-2004 (first entry)

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-5\_copy\_84\_147.rup.

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This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450-5\_copy\_84\_147.rup.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:19 ; Search time 150.72 Seconds  
(without alignments)  
392.788 Million cell updates/sec

Title: US-10-663-450-5\_COPY\_84\_147  
Perfect score: 323  
Sequence: 1 EKKPVKKRKSQVQLPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID           | Description        |
|------------|-------|---------|--------------|----|--------------|--------------------|
| 1          | 323   | 100.0   | 451          | 2  | Q8TFF3_TRIRE | Q8tff3 trichoderma |
| 2          | 319   | 98.8    | 430          | 2  | Q7SHF0_NEUCR | Q7shf0 neurospora  |
| 3          | 296   | 91.6    | 556          | 2  | Q2KH12_MAGGR | Q2kh12 magnaporthe |
| 4          | 292   | 90.4    | 342          | 2  | Q6W8X2_ASPNG | Q6w8x2 aspergillus |

|    |       |      |     |   |              |        |             |
|----|-------|------|-----|---|--------------|--------|-------------|
| 5  | 288   | 89.2 | 347 | 2 | Q5AQN3_EMENI | Q5aqn3 | aspergillus |
| 6  | 288   | 89.2 | 348 | 2 | Q2U743_ASPOR | Q2u743 | aspergillus |
| 7  | 288   | 89.2 | 350 | 2 | Q8TFU8_EMENI | Q8tfu8 | emericella  |
| 8  | 286   | 88.5 | 429 | 2 | Q4HTT5_GIBZE | Q4htt5 | gibberella  |
| 9  | 285   | 88.2 | 433 | 2 | Q4WEY8_ASPFU | Q4wey8 | aspergillus |
| 10 | 178   | 55.1 | 260 | 2 | Q6BQC2_DEBHA | Q6bqc2 | debaryomyce |
| 11 | 178   | 55.1 | 273 | 2 | Q6CKQ1_KLULA | Q6ckq1 | kluyveromyc |
| 12 | 175.5 | 54.3 | 299 | 2 | Q6CEV1_YARLI | Q6cev1 | yarrowia li |
| 13 | 175   | 54.2 | 230 | 1 | HAC1_YEAST   | P41546 | saccharomyc |
| 14 | 174   | 53.9 | 357 | 2 | Q5AA52_CANAL | Q5aa52 | candida alb |
| 15 | 168   | 52.0 | 228 | 2 | Q75BQ5_ASHGO | Q75bq5 | ashbya goss |
| 16 | 148   | 45.8 | 329 | 2 | Q6FLY3_CANGA | Q6fly3 | candida gla |
| 17 | 107   | 33.1 | 336 | 2 | Q5VR11_ORYSA | Q5vr11 | oryza sativ |
| 18 | 106   | 32.8 | 168 | 1 | HY5_ARATH    | O24646 | arabidopsis |
| 19 | 102   | 31.6 | 69  | 2 | Q58L60_BRACM | Q58l60 | brassica ca |
| 20 | 102   | 31.6 | 109 | 2 | Q84XX8_BRARP | Q84xx8 | brassica ra |
| 21 | 101   | 31.3 | 158 | 1 | HY5_LYCES    | Q9sm50 | lycopersico |
| 22 | 100.5 | 31.1 | 141 | 2 | Q677A7_HYAOR | Q677a7 | hyacinthus  |
| 23 | 98    | 30.3 | 176 | 2 | Q69XK6_ORYSA | Q69xk6 | oryza sativ |
| 24 | 96    | 29.7 | 252 | 2 | Q6NX18_XENTR | Q6nx18 | xenopus tro |
| 25 | 94    | 29.1 | 188 | 2 | Q6ZHT8_ORYSA | Q6zht8 | oryza sativ |
| 26 | 94    | 29.1 | 321 | 2 | Q8GRY7_LOTJA | Q8gry7 | lotus japon |
| 27 | 94    | 29.1 | 646 | 2 | Q6AU90_ORYSA | Q6au90 | oryza sativ |
| 28 | 94    | 29.1 | 686 | 2 | Q61D33_CAEBR | Q61d33 | caenorhabdi |
| 29 | 93    | 28.8 | 120 | 2 | Q682B6_ARATH | Q682b6 | arabidopsis |
| 30 | 93    | 28.8 | 149 | 1 | HYH_ARATH    | Q8w191 | arabidopsis |
| 31 | 92    | 28.5 | 254 | 2 | Q2TAU5_XENLA | Q2tau5 | xenopus lae |
| 32 | 92    | 28.5 | 350 | 2 | Q90ZR7_XENLA | Q90zr7 | xenopus lae |
| 33 | 92    | 28.5 | 396 | 2 | Q7ZYC2_XENLA | Q7zyc2 | xenopus lae |
| 34 | 92    | 28.5 | 460 | 2 | Q93XA0_PHAVU | Q93xa0 | phaseolus v |
| 35 | 91    | 28.2 | 322 | 2 | Q39896_SOYBN | Q39896 | glycine max |
| 36 | 91    | 28.2 | 326 | 2 | Q39895_SOYBN | Q39895 | glycine max |
| 37 | 90.5  | 28.0 | 690 | 2 | O44743_CAEEL | O44743 | caenorhabdi |
| 38 | 90    | 27.9 | 379 | 2 | Q3UNH6_MOUSE | Q3unh6 | m bone marr |
| 39 | 90    | 27.9 | 404 | 1 | CREB3_MOUSE  | Q61817 | mus musculu |
| 40 | 89    | 27.6 | 371 | 2 | Q5TCV1_HUMAN | Q5tcv1 | homo sapien |
| 41 | 89    | 27.6 | 371 | 2 | Q5R5Z9_PONPY | Q5r5z9 | pongo pygma |
| 42 | 89    | 27.6 | 395 | 1 | CREB3_HUMAN  | O43889 | homo sapien |
| 43 | 88.5  | 27.4 | 208 | 2 | Q5DFK2_SCHJA | Q5dfk2 | schistosoma |
| 44 | 88.5  | 27.4 | 437 | 2 | Q569T3_XENLA | Q569t3 | xenopus lae |
| 45 | 88    | 27.2 | 322 | 2 | O04234_VICFA | O04234 | vicia faba  |

## ALIGNMENTS

## RESULT 1

## Q8TFF3\_TRIRE

ID Q8TFF3\_TRIRE PRELIMINARY; PRT; 451 AA.

AC Q8TFF3;

DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2002, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Transcription factor.

GN Name=hacl;

OS Trichoderma reesei (Hypocrea jecorina).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

OX NCBI\_TaxID=51453;

RN [1]

RP NUCLEOTIDE SEQUENCE.

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rapbn.

|                            |                                      |                              |                       |                             |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| <a href="#">Score Home</a> | <a href="#">Retrieve Application</a> | <a href="#">SCORE System</a> | <a href="#">SCORE</a> | <a href="#">Comments /</a>  |
| <a href="#">Page</a>       | <a href="#">List</a>                 | <a href="#">Overview</a>     | <a href="#">FAQ</a>   | <a href="#">Suggestions</a> |

This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rapbn.

[start](#)

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:44:20 ; Search time 8.64 Seconds  
(without alignments)  
169.226 Million cell updates/sec

Title: US-10-663-450-6\_COPY\_53\_116  
Perfect score: 324  
Sequence: 1 KKPAAKKRKSQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        |            |
|--------|------------|
| Result | %<br>Query |
|--------|------------|

| No. | Score | Match | Length | DB | ID                  | Description       |
|-----|-------|-------|--------|----|---------------------|-------------------|
| 1   | 251   | 77.5  | 425    | 6  | US-10-449-902-40262 | Sequence 40262, A |
| 2   | 106   | 32.7  | 134    | 6  | US-10-953-349-13422 | Sequence 13422, A |
| 3   | 106   | 32.7  | 134    | 6  | US-10-953-349-22329 | Sequence 22329, A |
| 4   | 106   | 32.7  | 191    | 6  | US-10-953-349-13421 | Sequence 13421, A |
| 5   | 106   | 32.7  | 191    | 6  | US-10-953-349-22328 | Sequence 22328, A |
| 6   | 97    | 29.9  | 199    | 6  | US-10-953-349-12209 | Sequence 12209, A |
| 7   | 97    | 29.9  | 201    | 6  | US-10-953-349-20562 | Sequence 20562, A |
| 8   | 97    | 29.9  | 318    | 6  | US-10-953-349-12208 | Sequence 12208, A |
| 9   | 97    | 29.9  | 320    | 6  | US-10-953-349-20561 | Sequence 20561, A |
| 10  | 97    | 29.9  | 324    | 6  | US-10-953-349-12207 | Sequence 12207, A |
| 11  | 97    | 29.9  | 326    | 6  | US-10-953-349-20560 | Sequence 20560, A |
| 12  | 92    | 28.4  | 646    | 6  | US-10-449-902-51369 | Sequence 51369, A |
| 13  | 80.5  | 24.8  | 293    | 6  | US-10-953-349-23767 | Sequence 23767, A |
| 14  | 80.5  | 24.8  | 318    | 6  | US-10-953-349-23766 | Sequence 23766, A |
| 15  | 80.5  | 24.8  | 323    | 6  | US-10-953-349-23765 | Sequence 23765, A |
| 16  | 79.5  | 24.5  | 675    | 6  | US-10-449-902-42244 | Sequence 42244, A |
| 17  | 78    | 24.1  | 296    | 6  | US-10-953-349-24027 | Sequence 24027, A |
| 18  | 78    | 24.1  | 362    | 6  | US-10-953-349-24026 | Sequence 24026, A |
| 19  | 78    | 24.1  | 382    | 6  | US-10-953-349-24025 | Sequence 24025, A |
| 20  | 78    | 24.1  | 611    | 7  | US-11-321-421-81    | Sequence 81, Appl |
| 21  | 77    | 23.8  | 332    | 6  | US-10-953-349-23520 | Sequence 23520, A |
| 22  | 75.5  | 23.3  | 335    | 6  | US-10-449-902-34705 | Sequence 34705, A |
| 23  | 75.5  | 23.3  | 467    | 6  | US-10-449-902-38097 | Sequence 38097, A |
| 24  | 75.5  | 23.3  | 675    | 7  | US-11-293-697-3326  | Sequence 3326, Ap |
| 25  | 75    | 23.1  | 142    | 6  | US-10-449-902-31867 | Sequence 31867, A |
| 26  | 75    | 23.1  | 147    | 6  | US-10-953-349-36806 | Sequence 36806, A |
| 27  | 75    | 23.1  | 165    | 6  | US-10-953-349-36805 | Sequence 36805, A |
| 28  | 75    | 23.1  | 186    | 6  | US-10-953-349-36804 | Sequence 36804, A |
| 29  | 75    | 23.1  | 457    | 6  | US-10-449-902-53115 | Sequence 53115, A |
| 30  | 75    | 23.1  | 523    | 6  | US-10-449-902-56056 | Sequence 56056, A |
| 31  | 75    | 23.1  | 650    | 6  | US-10-449-902-44708 | Sequence 44708, A |
| 32  | 74    | 22.8  | 301    | 6  | US-10-449-902-43842 | Sequence 43842, A |
| 33  | 73    | 22.5  | 380    | 6  | US-10-449-902-43338 | Sequence 43338, A |
| 34  | 73    | 22.5  | 467    | 7  | US-11-293-697-3606  | Sequence 3606, Ap |
| 35  | 72.5  | 22.4  | 237    | 6  | US-10-953-349-34004 | Sequence 34004, A |
| 36  | 72.5  | 22.4  | 621    | 6  | US-10-449-902-45462 | Sequence 45462, A |
| 37  | 72.5  | 22.4  | 621    | 6  | US-10-449-902-52809 | Sequence 52809, A |
| 38  | 72    | 22.2  | 188    | 6  | US-10-449-902-39656 | Sequence 39656, A |
| 39  | 72    | 22.2  | 357    | 6  | US-10-449-902-50208 | Sequence 50208, A |
| 40  | 72    | 22.2  | 393    | 6  | US-10-449-902-41469 | Sequence 41469, A |
| 41  | 71    | 21.9  | 215    | 6  | US-10-449-902-45271 | Sequence 45271, A |
| 42  | 71    | 21.9  | 223    | 6  | US-10-449-902-31526 | Sequence 31526, A |
| 43  | 71    | 21.9  | 279    | 6  | US-10-953-349-25745 | Sequence 25745, A |
| 44  | 70.5  | 21.8  | 281    | 6  | US-10-971-483-2     | Sequence 2, Appli |
| 45  | 70    | 21.6  | 167    | 6  | US-10-449-902-40094 | Sequence 40094, A |

## ALIGNMENTS

## RESULT 1

US-10-449-902-40262

; Sequence 40262, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rapbm.

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[start](#)

[Go Back to previous page](#)

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:42:39 ; Search time 100.8 Seconds  
(without alignments)  
294.105 Million cell updates/sec

Title: US-10-663-450-6\_COPY\_53\_116  
Perfect score: 324  
Sequence: 1 KKPAKKRKSWGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| -----      |       |             |        |       |             |

|    |       |       |     |   |                      |                   |
|----|-------|-------|-----|---|----------------------|-------------------|
| 1  | 324   | 100.0 | 349 | 3 | US-09-816-277-4      | Sequence 4, Appli |
| 2  | 324   | 100.0 | 349 | 3 | US-09-816-277-6      | Sequence 6, Appli |
| 3  | 324   | 100.0 | 349 | 4 | US-10-663-450-4      | Sequence 4, Appli |
| 4  | 324   | 100.0 | 349 | 4 | US-10-663-450-6      | Sequence 6, Appli |
| 5  | 317   | 97.8  | 342 | 3 | US-09-816-277-19     | Sequence 19, Appl |
| 6  | 317   | 97.8  | 342 | 4 | US-10-663-450-19     | Sequence 19, Appl |
| 7  | 317   | 97.8  | 386 | 3 | US-09-816-277-16     | Sequence 16, Appl |
| 8  | 317   | 97.8  | 386 | 4 | US-10-663-450-16     | Sequence 16, Appl |
| 9  | 283   | 87.3  | 451 | 3 | US-09-816-277-2      | Sequence 2, Appli |
| 10 | 283   | 87.3  | 451 | 3 | US-09-816-277-5      | Sequence 5, Appli |
| 11 | 283   | 87.3  | 451 | 4 | US-10-663-450-2      | Sequence 2, Appli |
| 12 | 283   | 87.3  | 451 | 4 | US-10-663-450-5      | Sequence 5, Appli |
| 13 | 277   | 85.5  | 409 | 3 | US-09-533-029-104    | Sequence 104, App |
| 14 | 277   | 85.5  | 409 | 4 | US-10-295-403-158    | Sequence 158, App |
| 15 | 277   | 85.5  | 409 | 4 | US-10-412-699B-684   | Sequence 684, App |
| 16 | 250   | 77.2  | 174 | 4 | US-10-767-701-61238  | Sequence 61238, A |
| 17 | 171.5 | 52.9  | 200 | 4 | US-10-369-493-21867  | Sequence 21867, A |
| 18 | 170   | 52.5  | 68  | 3 | US-09-816-277-60     | Sequence 60, Appl |
| 19 | 170   | 52.5  | 68  | 4 | US-10-663-450-60     | Sequence 60, Appl |
| 20 | 117   | 36.1  | 203 | 4 | US-10-437-963-151695 | Sequence 151695,  |
| 21 | 117   | 36.1  | 203 | 5 | US-10-732-923-13694  | Sequence 13694, A |
| 22 | 117   | 36.1  | 203 | 5 | US-10-732-923-13695  | Sequence 13695, A |
| 23 | 116   | 35.8  | 168 | 3 | US-09-934-455-102    | Sequence 102, App |
| 24 | 116   | 35.8  | 168 | 4 | US-10-225-066A-206   | Sequence 206, App |
| 25 | 116   | 35.8  | 168 | 4 | US-10-374-780A-2356  | Sequence 2356, Ap |
| 26 | 116   | 35.8  | 168 | 5 | US-10-732-923-13692  | Sequence 13692, A |
| 27 | 116   | 35.8  | 168 | 5 | US-10-225-066A-206   | Sequence 206, App |
| 28 | 111.5 | 34.4  | 192 | 3 | US-09-772-656-2      | Sequence 2, Appli |
| 29 | 111.5 | 34.4  | 192 | 3 | US-09-772-656-6      | Sequence 6, Appli |
| 30 | 111.5 | 34.4  | 192 | 3 | US-09-772-656-10     | Sequence 10, Appl |
| 31 | 111.5 | 34.4  | 192 | 4 | US-10-396-199A-2     | Sequence 2, Appli |
| 32 | 111.5 | 34.4  | 192 | 4 | US-10-396-199A-6     | Sequence 6, Appli |
| 33 | 111.5 | 34.4  | 192 | 4 | US-10-396-199A-10    | Sequence 10, Appl |
| 34 | 111   | 34.3  | 147 | 4 | US-10-425-115-187302 | Sequence 187302,  |
| 35 | 109   | 33.6  | 109 | 5 | US-10-732-923-13697  | Sequence 13697, A |
| 36 | 109   | 33.6  | 196 | 4 | US-10-425-115-197786 | Sequence 197786,  |
| 37 | 108   | 33.3  | 176 | 4 | US-10-437-963-164243 | Sequence 164243,  |
| 38 | 106.5 | 32.9  | 170 | 4 | US-10-310-154-565    | Sequence 565, App |
| 39 | 104.5 | 32.3  | 191 | 4 | US-10-424-599-177263 | Sequence 177263,  |
| 40 | 104   | 32.1  | 181 | 5 | US-10-732-923-450    | Sequence 450, App |
| 41 | 101   | 31.2  | 217 | 4 | US-10-425-115-197783 | Sequence 197783,  |
| 42 | 100   | 30.9  | 143 | 5 | US-10-856-499-1930   | Sequence 1930, Ap |
| 43 | 99    | 30.6  | 114 | 4 | US-10-425-115-246430 | Sequence 246430,  |
| 44 | 99    | 30.6  | 360 | 4 | US-10-437-963-165206 | Sequence 165206,  |
| 45 | 98    | 30.2  | 149 | 5 | US-10-732-923-13693  | Sequence 13693, A |

#### ALIGNMENTS

##### RESULT 1

US-09-816-277-4

; Sequence 4, Application US/09816277

; Publication No. US20010034045A1

; GENERAL INFORMATION:

; APPLICANT: Penttila, Merja E.

; APPLICANT: Ward, Michael

; APPLICANT: Wang, Huaming

; APPLICANT: Valkonen, Mari J.

; APPLICANT: Saloheimo, Markku

; TITLE OF INVENTION: Increased Production of Secreted

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rai.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450-6\_copy\_53\_116.rai.

[start](#)

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:41:45 ; Search time 29.44 Seconds  
(without alignments)  
190.284 Million cell updates/sec

Title: US-10-663-450-6\_COPY\_53\_116  
Perfect score: 324  
Sequence: 1 KKPAAKKRKSWSGQELPVPKTN.....RAAAQTSRERKRLEMEKLES 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-------------|
| -----      |       |         |              |       |             |



|    |      |      |      |   |                      |                   |
|----|------|------|------|---|----------------------|-------------------|
| 1  | 277  | 85.5 | 409  | 2 | US-09-533-029-104    | Sequence 104, App |
| 2  | 166  | 51.2 | 248  | 2 | US-09-248-796A-18840 | Sequence 18840, A |
| 3  | 100  | 30.9 | 143  | 2 | US-09-640-211A-1930  | Sequence 1930, Ap |
| 4  | 91.5 | 28.2 | 102  | 2 | US-09-640-211A-1046  | Sequence 1046, Ap |
| 5  | 91   | 28.1 | 264  | 2 | US-09-949-016-10789  | Sequence 10789, A |
| 6  | 87.5 | 27.0 | 260  | 2 | US-09-538-092-950    | Sequence 950, App |
| 7  | 86   | 26.5 | 667  | 2 | US-09-248-796A-14492 | Sequence 14492, A |
| 8  | 84.5 | 26.1 | 521  | 1 | US-08-721-684C-2     | Sequence 2, Appli |
| 9  | 84.5 | 26.1 | 521  | 1 | US-09-005-970-2      | Sequence 2, Appli |
| 10 | 84.5 | 26.1 | 521  | 2 | US-09-407-715-2      | Sequence 2, Appli |
| 11 | 83   | 25.6 | 23   | 2 | US-09-831-642-72     | Sequence 72, Appl |
| 12 | 80   | 24.7 | 212  | 2 | US-09-489-039A-13074 | Sequence 13074, A |
| 13 | 79   | 24.4 | 63   | 2 | US-09-107-433-3674   | Sequence 3674, Ap |
| 14 | 78   | 24.1 | 611  | 2 | US-09-216-393B-81    | Sequence 81, Appl |
| 15 | 77.5 | 23.9 | 1601 | 2 | US-09-345-473E-40    | Sequence 40, Appl |
| 16 | 77.5 | 23.9 | 1601 | 2 | US-09-862-027-40     | Sequence 40, Appl |
| 17 | 76.5 | 23.6 | 306  | 2 | US-09-758-759-115    | Sequence 115, App |
| 18 | 76.5 | 23.6 | 395  | 2 | US-09-247-155-113    | Sequence 113, App |
| 19 | 76.5 | 23.6 | 395  | 2 | US-09-513-999C-14    | Sequence 14, Appl |
| 20 | 76.5 | 23.6 | 395  | 2 | US-09-471-276-14     | Sequence 14, Appl |
| 21 | 76.5 | 23.6 | 395  | 2 | US-09-903-190-113    | Sequence 113, App |
| 22 | 75.5 | 23.3 | 351  | 2 | US-09-870-089B-2     | Sequence 2, Appli |
| 23 | 75.5 | 23.3 | 362  | 2 | US-09-949-016-10923  | Sequence 10923, A |
| 24 | 75.5 | 23.3 | 501  | 2 | US-09-949-016-11281  | Sequence 11281, A |
| 25 | 75.5 | 23.3 | 931  | 2 | US-09-949-016-9850   | Sequence 9850, Ap |
| 26 | 74.5 | 23.0 | 338  | 1 | US-08-218-686-2      | Sequence 2, Appli |
| 27 | 74.5 | 23.0 | 338  | 2 | US-08-460-242-2      | Sequence 2, Appli |
| 28 | 74.5 | 23.0 | 452  | 2 | US-09-949-016-7289   | Sequence 7289, Ap |
| 29 | 74   | 22.8 | 616  | 2 | US-09-873-404-4      | Sequence 4, Appli |
| 30 | 74   | 22.8 | 616  | 2 | US-10-243-735-4      | Sequence 4, Appli |
| 31 | 74   | 22.8 | 616  | 2 | US-10-730-010-4      | Sequence 4, Appli |
| 32 | 73   | 22.5 | 551  | 2 | US-08-796-899-29     | Sequence 29, Appl |
| 33 | 73   | 22.5 | 1637 | 2 | US-09-718-692-2      | Sequence 2, Appli |
| 34 | 73   | 22.5 | 1637 | 2 | US-09-718-852-2      | Sequence 2, Appli |
| 35 | 73   | 22.5 | 1637 | 2 | US-09-718-815-2      | Sequence 2, Appli |
| 36 | 72.5 | 22.4 | 371  | 2 | US-09-148-545-259    | Sequence 259, App |
| 37 | 72.5 | 22.4 | 371  | 2 | US-09-621-011-259    | Sequence 259, App |
| 38 | 72   | 22.2 | 645  | 2 | US-09-949-016-11022  | Sequence 11022, A |
| 39 | 72   | 22.2 | 650  | 2 | US-09-487-558B-430   | Sequence 430, App |
| 40 | 72   | 22.2 | 700  | 2 | US-09-831-642-34     | Sequence 34, Appl |
| 41 | 71   | 21.9 | 325  | 2 | US-09-267-031-14     | Sequence 14, Appl |
| 42 | 71   | 21.9 | 802  | 2 | US-09-823-240A-2     | Sequence 2, Appli |
| 43 | 70.5 | 21.8 | 118  | 2 | US-09-134-001C-2856  | Sequence 2856, Ap |
| 44 | 70.5 | 21.8 | 182  | 2 | US-09-640-211A-800   | Sequence 800, App |
| 45 | 70.5 | 21.8 | 307  | 2 | US-09-267-031-6      | Sequence 6, Appli |

#### ALIGNMENTS

##### RESULT 1

US-09-533-029-104

; Sequence 104, Application US/09533029

; Patent No. 6664446

; GENERAL INFORMATION:

; APPLICANT: Heard, Jacqueline

; APPLICANT: Broun, Pierre

; APPLICANT: Riechmann, Jose-Luis

; APPLICANT: Keddie, James

; APPLICANT: Pineda, Omaira

; APPLICANT: Adam, Luc

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This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450  
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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:33:51 ; Search time 18.56 Seconds  
(without alignments)  
331.782 Million cell updates/sec

Title: US-10-663-450-5\_COPY\_84\_147  
Perfect score: 323  
Sequence: 1 EKKPVKKRKSWSGQVLPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | % Query |        | DB | ID     | Description        |
|------------|-------|---------|--------|----|--------|--------------------|
|            |       | Match   | Length |    |        |                    |
| 1          | 175   | 54.2    | 238    | 2  | S78571 | transcription fact |
| 2          | 106   | 32.8    | 168    | 2  | T50922 | bZIP protein HY5 [ |
| 3          | 91    | 28.2    | 322    | 2  | T08592 | TGACG-motif-bindin |
| 4          | 91    | 28.2    | 326    | 2  | T08591 | TGACG-motif bindin |
| 5          | 90.5  | 28.0    | 688    | 2  | T32750 | hypothetical prote |
| 6          | 88    | 27.2    | 322    | 2  | T12093 | TGACG-motif bindin |
| 7          | 87.5  | 27.1    | 176    | 2  | B90087 | hypothetical prote |
| 8          | 87    | 26.9    | 600    | 2  | T00759 | hypothetical prote |

|    |      |      |      |   |        |                    |
|----|------|------|------|---|--------|--------------------|
| 9  | 86   | 26.6 | 360  | 2 | T03373 | probable G-box bin |
| 10 | 81   | 25.1 | 445  | 2 | T50972 | probable zuotin [i |
| 11 | 80.5 | 24.9 | 486  | 2 | JC4028 | activating transcr |
| 12 | 79.5 | 24.6 | 2052 | 2 | T18519 | myosin X - bovine  |
| 13 | 79   | 24.5 | 381  | 2 | S26812 | transcription fact |
| 14 | 79   | 24.5 | 672  | 2 | T21469 | hypothetical prote |
| 15 | 78.5 | 24.3 | 232  | 2 | S42392 | G-box-binding prot |
| 16 | 78.5 | 24.3 | 242  | 2 | S05453 | transcription fact |
| 17 | 78   | 24.1 | 424  | 2 | T10985 | regulator protein  |
| 18 | 77.5 | 24.0 | 246  | 2 | T12585 | Dc3 promoter-bindi |
| 19 | 77.5 | 24.0 | 483  | 2 | S12741 | transcription fact |
| 20 | 77.5 | 24.0 | 505  | 1 | S05380 | transcription fact |
| 21 | 77   | 23.8 | 1089 | 2 | T36663 | protein kinase, tr |
| 22 | 76.5 | 23.7 | 144  | 2 | T14796 | hypothetical prote |
| 23 | 76.5 | 23.7 | 313  | 2 | A34785 | DNA-binding protei |
| 24 | 76.5 | 23.7 | 351  | 2 | A45377 | transcription fact |
| 25 | 76.5 | 23.7 | 358  | 2 | C42026 | cyclic AMP respons |
| 26 | 76.5 | 23.7 | 389  | 1 | A39429 | cAMP response elem |
| 27 | 76.5 | 23.7 | 448  | 2 | A42026 | cAMP response elem |
| 28 | 76.5 | 23.7 | 456  | 2 | B42026 | cyclic AMP respons |
| 29 | 76   | 23.5 | 502  | 2 | T20130 | hypothetical prote |
| 30 | 76   | 23.5 | 521  | 2 | S06218 | colicin E1 - Shige |
| 31 | 76   | 23.5 | 838  | 2 | T20125 | hypothetical prote |
| 32 | 75.5 | 23.4 | 315  | 2 | S20883 | G-box-binding fact |
| 33 | 75.5 | 23.4 | 315  | 2 | G85433 | G-box-binding fact |
| 34 | 75.5 | 23.4 | 605  | 2 | T02350 | hypothetical prote |
| 35 | 75   | 23.2 | 267  | 2 | JC4857 | hepatocarcinogenes |
| 36 | 75   | 23.2 | 267  | 2 | S51307 | G-box binding fact |
| 37 | 75   | 23.2 | 433  | 2 | JC1230 | DNA-binding protei |
| 38 | 75   | 23.2 | 761  | 2 | T00940 | hypothetical prote |
| 39 | 75   | 23.2 | 2062 | 2 | A59297 | myosin X - mouse   |
| 40 | 74.5 | 23.1 | 313  | 2 | S66312 | G-box binding fact |
| 41 | 74.5 | 23.1 | 349  | 2 | A41349 | histone-specific t |
| 42 | 74.5 | 23.1 | 349  | 2 | S77570 | transcription fact |
| 43 | 74.5 | 23.1 | 452  | 2 | H96710 | hypothetical prote |
| 44 | 74   | 22.9 | 331  | 2 | T26807 | hypothetical prote |
| 45 | 74   | 22.9 | 333  | 2 | T26808 | hypothetical prote |

#### ALIGNMENTS

##### RESULT 1

S78571

transcription factor HAC1 - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein YFL031w

C;Species: *Saccharomyces cerevisiae*

C;Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004

C;Accession: S78571; S56223; S53578

R;Murakami, Y.

submitted to the Protein Sequence Database, January 1998

A;Reference number: S78570

A;Accession: S78571

A;Molecule type: DNA

A;Residues: 1-238

A;Cross-references: UNIPROT:P41546; UNIPARC:UPI0000157F61; EMBL:D50617; MIPS:YFL031w

A;Note: this is a revision to the sequence from reference S56186

R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasa submitted to the EMBL Data Library, May 1995

A;Description: Analysis of the nucleotide sequence of chromosome VI from *Saccaromyces*

A;Reference number: S56186

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-5\_copy\_84\_147.rapbn.

|                            |                                      |                              |                       |                             |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| <a href="#">Score Home</a> | <a href="#">Retrieve Application</a> | <a href="#">SCORE System</a> | <a href="#">SCORE</a> | <a href="#">Comments /</a>  |
| <a href="#">Page</a>       | <a href="#">List</a>                 | <a href="#">Overview</a>     | <a href="#">FAQ</a>   | <a href="#">Suggestions</a> |

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:44:20 ; Search time 8.64 Seconds  
(without alignments)  
169.226 Million cell updates/sec

Title: US-10-663-450-5\_COPY\_84\_147  
Perfect score: 323  
Sequence: 1 EKKFPVKRKSQVLPPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        |            |
|--------|------------|
| Result | %<br>Query |
|--------|------------|

| No. | Score | Match | Length | DB | ID                  | Description       |
|-----|-------|-------|--------|----|---------------------|-------------------|
| 1   | 269   | 83.3  | 425    | 6  | US-10-449-902-40262 | Sequence 40262, A |
| 2   | 103.5 | 32.0  | 134    | 6  | US-10-953-349-13422 | Sequence 13422, A |
| 3   | 103.5 | 32.0  | 134    | 6  | US-10-953-349-22329 | Sequence 22329, A |
| 4   | 103.5 | 32.0  | 191    | 6  | US-10-953-349-13421 | Sequence 13421, A |
| 5   | 103.5 | 32.0  | 191    | 6  | US-10-953-349-22328 | Sequence 22328, A |
| 6   | 94    | 29.1  | 646    | 6  | US-10-449-902-51369 | Sequence 51369, A |
| 7   | 91    | 28.2  | 199    | 6  | US-10-953-349-12209 | Sequence 12209, A |
| 8   | 91    | 28.2  | 201    | 6  | US-10-953-349-20562 | Sequence 20562, A |
| 9   | 91    | 28.2  | 318    | 6  | US-10-953-349-12208 | Sequence 12208, A |
| 10  | 91    | 28.2  | 320    | 6  | US-10-953-349-20561 | Sequence 20561, A |
| 11  | 91    | 28.2  | 324    | 6  | US-10-953-349-12207 | Sequence 12207, A |
| 12  | 91    | 28.2  | 326    | 6  | US-10-953-349-20560 | Sequence 20560, A |
| 13  | 88    | 27.2  | 296    | 6  | US-10-953-349-24027 | Sequence 24027, A |
| 14  | 88    | 27.2  | 362    | 6  | US-10-953-349-24026 | Sequence 24026, A |
| 15  | 88    | 27.2  | 382    | 6  | US-10-953-349-24025 | Sequence 24025, A |
| 16  | 82.5  | 25.5  | 611    | 7  | US-11-321-421-81    | Sequence 81, Appl |
| 17  | 81    | 25.1  | 335    | 6  | US-10-449-902-34705 | Sequence 34705, A |
| 18  | 80.5  | 24.9  | 293    | 6  | US-10-953-349-23767 | Sequence 23767, A |
| 19  | 80.5  | 24.9  | 318    | 6  | US-10-953-349-23766 | Sequence 23766, A |
| 20  | 80.5  | 24.9  | 323    | 6  | US-10-953-349-23765 | Sequence 23765, A |
| 21  | 78    | 24.1  | 142    | 6  | US-10-449-902-31867 | Sequence 31867, A |
| 22  | 77    | 23.8  | 380    | 6  | US-10-449-902-43338 | Sequence 43338, A |
| 23  | 75.5  | 23.4  | 281    | 6  | US-10-971-483-2     | Sequence 2, Appli |
| 24  | 75    | 23.2  | 332    | 6  | US-10-953-349-23520 | Sequence 23520, A |
| 25  | 75    | 23.2  | 553    | 6  | US-10-449-902-47325 | Sequence 47325, A |
| 26  | 74.5  | 23.1  | 237    | 6  | US-10-953-349-34004 | Sequence 34004, A |
| 27  | 73.5  | 22.8  | 115    | 6  | US-10-449-902-29417 | Sequence 29417, A |
| 28  | 73    | 22.6  | 167    | 6  | US-10-449-902-40094 | Sequence 40094, A |
| 29  | 73    | 22.6  | 457    | 6  | US-10-449-902-53115 | Sequence 53115, A |
| 30  | 73    | 22.6  | 523    | 6  | US-10-449-902-56056 | Sequence 56056, A |
| 31  | 72    | 22.3  | 188    | 6  | US-10-449-902-39656 | Sequence 39656, A |
| 32  | 71    | 22.0  | 393    | 6  | US-10-449-902-41469 | Sequence 41469, A |
| 33  | 70.5  | 21.8  | 282    | 6  | US-10-511-937-2600  | Sequence 2600, Ap |
| 34  | 70.5  | 21.8  | 467    | 6  | US-10-449-902-38097 | Sequence 38097, A |
| 35  | 70.5  | 21.8  | 539    | 6  | US-10-449-902-54234 | Sequence 54234, A |
| 36  | 70.5  | 21.8  | 784    | 6  | US-10-449-902-41427 | Sequence 41427, A |
| 37  | 70    | 21.7  | 279    | 6  | US-10-953-349-25745 | Sequence 25745, A |
| 38  | 70    | 21.7  | 400    | 6  | US-10-449-902-39710 | Sequence 39710, A |
| 39  | 69.5  | 21.5  | 282    | 6  | US-10-953-349-37838 | Sequence 37838, A |
| 40  | 69.5  | 21.5  | 308    | 6  | US-10-953-349-37837 | Sequence 37837, A |
| 41  | 69.5  | 21.5  | 315    | 6  | US-10-953-349-37836 | Sequence 37836, A |
| 42  | 69.5  | 21.5  | 330    | 6  | US-10-449-902-53842 | Sequence 53842, A |
| 43  | 69.5  | 21.5  | 888    | 6  | US-10-449-902-47557 | Sequence 47557, A |
| 44  | 69    | 21.4  | 156    | 6  | US-10-953-349-25746 | Sequence 25746, A |
| 45  | 69    | 21.4  | 304    | 6  | US-10-449-902-38130 | Sequence 38130, A |

## ALIGNMENTS

## RESULT 1

US-10-449-902-40262

; Sequence 40262, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

# SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-5\_copy\_84\_147.rapbm.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:42:39 ; Search time 100.8 Seconds  
(without alignments)  
294.105 Million cell updates/sec

Title: US-10-663-450-5\_COPY\_84\_147  
Perfect score: 323  
Sequence: 1 EKKPVKKRKSQVLPEPKT.....NRRAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Score | Match | Length | DB | ID | Description |
|--------|-------|-------|--------|----|----|-------------|
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|    |       |       |     |   |                      |                   |
|----|-------|-------|-----|---|----------------------|-------------------|
| 1  | 323   | 100.0 | 451 | 3 | US-09-816-277-2      | Sequence 2, Appli |
| 2  | 323   | 100.0 | 451 | 3 | US-09-816-277-5      | Sequence 5, Appli |
| 3  | 323   | 100.0 | 451 | 4 | US-10-663-450-2      | Sequence 2, Appli |
| 4  | 323   | 100.0 | 451 | 4 | US-10-663-450-5      | Sequence 5, Appli |
| 5  | 307   | 95.0  | 409 | 3 | US-09-533-029-104    | Sequence 104, App |
| 6  | 307   | 95.0  | 409 | 4 | US-10-295-403-158    | Sequence 158, App |
| 7  | 307   | 95.0  | 409 | 4 | US-10-412-699B-684   | Sequence 684, App |
| 8  | 292   | 90.4  | 342 | 3 | US-09-816-277-19     | Sequence 19, Appl |
| 9  | 292   | 90.4  | 342 | 4 | US-10-663-450-19     | Sequence 19, Appl |
| 10 | 292   | 90.4  | 386 | 3 | US-09-816-277-16     | Sequence 16, Appl |
| 11 | 292   | 90.4  | 386 | 4 | US-10-663-450-16     | Sequence 16, Appl |
| 12 | 288   | 89.2  | 349 | 3 | US-09-816-277-4      | Sequence 4, Appli |
| 13 | 288   | 89.2  | 349 | 3 | US-09-816-277-6      | Sequence 6, Appli |
| 14 | 288   | 89.2  | 349 | 4 | US-10-663-450-4      | Sequence 4, Appli |
| 15 | 288   | 89.2  | 349 | 4 | US-10-663-450-6      | Sequence 6, Appli |
| 16 | 268   | 83.0  | 174 | 4 | US-10-767-701-61238  | Sequence 61238, A |
| 17 | 175   | 54.2  | 68  | 3 | US-09-816-277-60     | Sequence 60, Appl |
| 18 | 175   | 54.2  | 68  | 4 | US-10-663-450-60     | Sequence 60, Appl |
| 19 | 175   | 54.2  | 200 | 4 | US-10-369-493-21867  | Sequence 21867, A |
| 20 | 108   | 33.4  | 147 | 4 | US-10-425-115-187302 | Sequence 187302,  |
| 21 | 108   | 33.4  | 192 | 3 | US-09-772-656-2      | Sequence 2, Appli |
| 22 | 108   | 33.4  | 192 | 3 | US-09-772-656-6      | Sequence 6, Appli |
| 23 | 108   | 33.4  | 192 | 3 | US-09-772-656-10     | Sequence 10, Appl |
| 24 | 108   | 33.4  | 192 | 4 | US-10-396-199A-2     | Sequence 2, Appli |
| 25 | 108   | 33.4  | 192 | 4 | US-10-396-199A-6     | Sequence 6, Appli |
| 26 | 108   | 33.4  | 192 | 4 | US-10-396-199A-10    | Sequence 10, Appl |
| 27 | 107   | 33.1  | 203 | 4 | US-10-437-963-151695 | Sequence 151695,  |
| 28 | 107   | 33.1  | 203 | 5 | US-10-732-923-13694  | Sequence 13694, A |
| 29 | 107   | 33.1  | 203 | 5 | US-10-732-923-13695  | Sequence 13695, A |
| 30 | 106   | 32.8  | 168 | 3 | US-09-934-455-102    | Sequence 102, App |
| 31 | 106   | 32.8  | 168 | 4 | US-10-225-066A-206   | Sequence 206, App |
| 32 | 106   | 32.8  | 168 | 4 | US-10-374-780A-2356  | Sequence 2356, Ap |
| 33 | 106   | 32.8  | 168 | 5 | US-10-732-923-13692  | Sequence 13692, A |
| 34 | 106   | 32.8  | 168 | 5 | US-10-225-066A-206   | Sequence 206, App |
| 35 | 103.5 | 32.0  | 191 | 4 | US-10-424-599-177263 | Sequence 177263,  |
| 36 | 103   | 31.9  | 170 | 4 | US-10-310-154-565    | Sequence 565, App |
| 37 | 102   | 31.6  | 109 | 5 | US-10-732-923-13697  | Sequence 13697, A |
| 38 | 102   | 31.6  | 196 | 4 | US-10-425-115-197786 | Sequence 197786,  |
| 39 | 101   | 31.3  | 665 | 4 | US-10-425-115-190929 | Sequence 190929,  |
| 40 | 101   | 31.3  | 672 | 4 | US-10-425-114-58469  | Sequence 58469, A |
| 41 | 99    | 30.7  | 143 | 5 | US-10-856-499-1930   | Sequence 1930, Ap |
| 42 | 98    | 30.3  | 176 | 4 | US-10-437-963-164243 | Sequence 164243,  |
| 43 | 97    | 30.0  | 181 | 5 | US-10-732-923-450    | Sequence 450, App |
| 44 | 95    | 29.4  | 217 | 4 | US-10-425-115-197783 | Sequence 197783,  |
| 45 | 94    | 29.1  | 114 | 4 | US-10-425-115-246430 | Sequence 246430,  |

## ALIGNMENTS

## RESULT 1

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; Sequence 2, Application US/09816277

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